



CIBT-P01-130SequenceListing  
SEQUENCE LISTING

<110> Huston, J.  
Houston, L.L.  
Ring, D.  
Oppermann, H.

<120> BIOSYNTHETIC BINDING PROTEINS FOR IMMUNO-TARGETING

<130> CIBT-P01-130

<140> 09/558,741

<141> 2000-04-26

<150> 07/831,967

<151> 1992-02-06

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 909

<212> DNA

<213> Artificial Sequence

<220>

<223> 741F8 sFv'

<220>

<221> CDS

<222> (3)..(752)

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Met Ala Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys  
1 5 10 15

cct gga gag aca gtc aag atc tcc tgc aag gct tct ggg tat acc ttc 95  
Pro Gly Glu Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe  
20 25 30

aca aac tat gga atg aac tgg gtg aag cag gct cca gga aag ggt tta 143  
Thr Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu  
35 40 45

aag tgg atg ggc tgg ata aac acc aac act gga gag cca aca tat gct 191  
Lys Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala  
50 55 60

gaa gag ttc aag gga cgg ttt gcc ttc tct ttg gaa acc tct gcc agc 239  
Glu Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser  
65 70 75

act gcc tat ttg cag atc aag aag ctc aaa aat gag gac acg gct aca 287  
Thr Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr  
80 85 90 95

tat ttc tgt gga agg caa ttt att acc tac ggc ggg ttt gct aac tgg 335  
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Tyr	Phe	Cys	Gly	Arg	Gln	Phe	Ile	Thr	Tyr	Gly	Gly	Phe	Ala	Asn	Trp		
				100					105					110			
ggc	caa	ggg	act	ctg	gtc	act	gtc	tct	gca	tcg	agc	tcc	tcc	gga	tct	383	
Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Ser	Ser	Ser	Ser	Gly	Ser		
			115					120					125				
tca	tct	agc	ggt	tcc	agc	tcg	agc	gat	atc	gtc	atg	acc	cag	tct	cct	431	
Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Asp	Ile	Val	Met	Thr	Gln	Ser	Pro		
			130					135				140					
aaa	ttc	atg	tcc	acg	tca	gtg	gga	gac	agg	gtc	agc	atc	tcc	tgc	aag	479	
Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Ile	Ser	Cys	Lys		
	145					150					155						
gcc	agt	cag	gat	gtg	agt	act	gct	gta	gcc	tgg	tat	caa	caa	aaa	cca	527	
Ala	Ser	Gln	Asp	Val	Ser	Thr	Ala	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro		
						165				170					175		
ggg	caa	tct	cct	aaa	cta	ctg	att	tac	tgg	aca	tcc	acc	cgg	cac	act	575	
Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Thr	Ser	Thr	Arg	His	Thr		
				180					185					190			
gga	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct	ggg	aca	gat	tat	act	623	
Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Thr		
			195					200					205				
ctc	acc	atc	agc	agt	gtg	cag	gct	gaa	gac	ctg	gca	ctt	cat	tac	tgt	671	
Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu	Ala	Leu	His	Tyr	Cys		
			210				215					220					
cag	caa	cat	tat	aga	gtg	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg	719	
Gln	Gln	His	Tyr	Arg	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu		
	225					230					235						
gag	ata	aaa	cgg	gct	gat	ggg	gga	ggg	gga	tgt	taac	ggggga	ggtg	gatg	tt	772	
Glu	Ile	Lys	Arg	Ala	Asp	Gly	Gly	Gly	Gly	Cys							
	240				245					250							
gggtctcgtt	acgttg	cggga	tctcg	aggct	atcttt	tacta	actctt	accg	taaagt	ttctg						832	
gctcaactgt	ctgcac	gcaa	gctttt	gcag	gatatc	atga	gcgctt	aaga	tccgtc	gacc						892	
tgcagg	catg	caag	ctt													909	

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<220>  
 <223> 741F8 sFv'

<400> 2

Met	Ala	Glu	Ile	Gln	Leu	Val	Gln	Ser	Gly	Pro	Glu	Leu	Lys	Lys	Pro
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Gly	Glu	Thr	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe	Thr
			20					25					30		

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Asn Tyr Gly Met Asn Trp Val Lys Gln Ala Pro Gly Lys Gly Leu Lys  
 35 40 45  
 Trp Met Gly Trp Ile Asn Thr Asn Thr Gly Glu Pro Thr Tyr Ala Glu  
 50 55 60  
 Glu Phe Lys Gly Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Ser Thr  
 65 70 75 80  
 Ala Tyr Leu Gln Ile Lys Lys Leu Lys Asn Glu Asp Thr Ala Thr Tyr  
 85 90 95  
 Phe Cys Gly Arg Gln Phe Ile Thr Tyr Gly Gly Phe Ala Asn Trp Gly  
 100 105 110  
 Gln Gly Thr Leu Val Thr Val Ser Ala Ser Ser Ser Ser Gly Ser Ser  
 115 120 125  
 Ser Ser Gly Ser Ser Ser Ser Asp Ile Val Met Thr Gln Ser Pro Lys  
 130 135 140  
 Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Ser Cys Lys Ala  
 145 150 155 160  
 Ser Gln Asp Val Ser Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro Gly  
 165 170 175  
 Gln Ser Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly  
 180 185 190  
 Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu  
 195 200 205  
 Thr Ile Ser Ser Val Gln Ala Glu Asp Leu Ala Leu His Tyr Cys Gln  
 210 215 220  
 Gln His Tyr Arg Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu  
 225 230 235 240  
 Ile Lys Arg Ala Asp Gly Gly Gly Gly Cys  
 245 250

<210> 3  
 <211> 779  
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## CIBT-P01-130SequenceListing

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 <222> (3)..(758)  
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 ggc gcc tct gtg cgc atg tcc tgc aaa tcc tct ggg tac att ttc acc 95  
 Gly Ala Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr  
 20 25 30  
 gac ttc tac atg aat tgg gtt cgc cag tct cat ggt aag tct cta gac 143  
 Asp Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp  
 35 40 45  
 tac atc ggg tac att tcc cca tac tct ggg gtt acc ggc tac aac cag 191  
 Tyr Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln  
 50 55 60  
 aag ttt aaa ggt aag gcg acc ctt act gtc gac aaa tct tcc tca act 239  
 Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr  
 65 70 75  
 gct tac atg gag ctg cgt tct ttg acc tct gag gac tcc gcg gta tac 287  
 Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr  
 80 85 90 95  
 tat tgc gcg ggc tcc tct ggt aac aaa tgg gcc atg gat tat tgg ggt 335  
 Tyr Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly  
 100 105 110  
 cat ggt gct agc gtt act gtg agc tcc tcc gga tct tca tct agc ggt 383  
 His Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly  
 115 120 125  
 tcc agc tcg agt gga tcc gac gtc gta atg acc cag act ccg ctg tct 431  
 Ser Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser  
 130 135 140  
 ctg ccg gtt tct ctg ggt gac cag gct tct att tct tgc gcg tct tcc 479  
 Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser  
 145 150 155  
 cag tct ctg gtc cat tct aat ggt aac act tac ctg aac tgg tac ctg 527  
 Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu  
 160 165 170 175  
 caa aag gct ggt cag tct ccg aag ctt ctg atc tac aaa gtc tct aac 575  
 Gln Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn  
 180 185 190  
 cgc ttc tct ggt gtc ccg gat cgt ttc tct ggt tct ggt tct ggt act 623  
 Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 195 200 205  
 gac ttc acc ctg aag atc tct cgt gtc cag gcc gaa gac ctg ggt atc 671  
 Asp Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile

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210  
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 220  
 tac ttc tgc tct cag act act cat gta ccg ccg act ttt ggt ggt ggc 719  
 Tyr Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly  
 225 230 235  
 acc aag ctc gag att aaa cgt tcc ggg gga ggt gga tgt taactgcagc 768  
 Thr Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys  
 240 245 250  
 ccgggggatc c 779  
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 20 25 30  
 Phe Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr  
 35 40 45  
 Ile Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys  
 50 55 60  
 Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala  
 65 70 75 80  
 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
 85 90 95  
 Cys Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His  
 100 105 110  
 Gly Ala Ser Val Thr Val Ser Ser Ser Gly Ser Ser Ser Ser Gly Ser  
 115 120 125  
 Ser Ser Ser Gly Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu  
 130 135 140  
 Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln  
 145 150 155 160

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Ser Leu Val His Ser Asn Gly Asn Thr Tyr Leu Asn Trp Tyr Leu Gln  
165 170 175

Lys Ala Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg  
180 185 190

Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
195 200 205

Phe Thr Leu Lys Ile Ser Arg Val Gln Ala Glu Asp Leu Gly Ile Tyr  
210 215 220

Phe Cys Ser Gln Thr Thr His Val Pro Pro Thr Phe Gly Gly Gly Thr  
225 230 235 240

Lys Leu Glu Ile Lys Arg Ser Gly Gly Gly Gly Cys  
245 250

<210> 5  
<211> 739  
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<223> 520C9 sFv

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Glu Ile Gln Leu Val Gln Ser Gly Pro Glu Leu Lys Lys Pro Gly Glu  
1 5 10 15

aca gtc aag atc tcc tgc aag gct tct gga tat acc ttc gca aac tat 96  
Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr  
20 25 30

gga atg aac tgg atg aag cag gct cca gga aag ggt tta aag tgg atg 144  
Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
35 40 45

ggc tgg ata aac acc tac act gga cag tca aca tat gct gat gac ttc 192  
Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe  
50 55 60

aag gaa cgg ttt gcc ttc tct ttg gaa acc tct gcc acc act gcc cat 240  
Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His  
65 70 75 80

ttg cag atc aac aac ctc aga aat gag gac tcg gcc aca tat ttc tgt 288  
Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys

## CIBT-P01-130SequenceListing

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90

95

gca	aga	cga	ttt	ggg	ttt	gct	tac	tgg	ggc	caa	ggg	act	ctg	gtc	agt	336
Ala	Arg	Arg	Phe	Gly	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Ser	
			100					105					110			
gtc	tct	gca	tcg	ata	tcg	agc	tcc	tcc	gga	tct	tca	tct	agc	ggg	tcc	384
Val	Ser	Ala	Ser	Ile	Ser	Ser	Ser	Ser	Gly	Ser	Ser	Ser	Ser	Gly	Ser	
		115					120					125				
agc	tcg	agt	gga	tcc	gat	atc	cag	atg	acc	cag	tct	cca	tcc	tcc	tta	432
Ser	Ser	Ser	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	
		130				135					140					
tct	gcc	tct	ctg	gga	gaa	aga	gtc	agt	ctc	act	tgt	cgg	gca	agt	cag	480
Ser	Ala	Ser	Leu	Gly	Glu	Arg	Val	Ser	Leu	Thr	Cys	Arg	Ala	Ser	Gln	
					150					155					160	
gac	att	ggg	aat	agc	tta	acc	tgg	ctt	cag	cag	gaa	cca	gat	gga	act	528
Asp	Ile	Gly	Asn	Ser	Leu	Thr	Trp	Leu	Gln	Gln	Glu	Pro	Asp	Gly	Thr	
				165					170					175		
att	aaa	cgc	ctg	atc	tac	gcc	aca	tcc	agt	tta	gat	tct	ggg	gtc	ccc	576
Ile	Lys	Arg	Leu	Ile	Tyr	Ala	Thr	Ser	Ser	Leu	Asp	Ser	Gly	Val	Pro	
			180					185					190			
aaa	agg	ttc	agt	ggc	agt	cgg	tct	ggg	tca	gat	tat	tct	ctc	acc	atc	624
Lys	Arg	Phe	Ser	Gly	Ser	Arg	Ser	Gly	Ser	Asp	Tyr	Ser	Leu	Thr	Ile	
		195					200					205				
agt	agc	ctt	gag	tct	gaa	gat	ttt	gta	gtc	tat	tac	tgt	cta	caa	tat	672
Ser	Ser	Leu	Glu	Ser	Glu	Asp	Phe	Val	Val	Tyr	Tyr	Cys	Leu	Gln	Tyr	
		210				215				220						
gct	att	ttt	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aac	ctg	gaa	ata	aaa	720
Ala	Ile	Phe	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Asn	Leu	Glu	Ile	Lys	
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cgg	gct	gat	taatctgcag													739
Arg	Ala	Asp														

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<220>  
 <223> 520C9 sFV

<400> 6

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 1 5 10 15

Thr Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr  
 20 25 30

Gly Met Asn Trp Met Lys Gln Ala Pro Gly Lys Gly Leu Lys Trp Met  
 35 40 45

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Gly Trp Ile Asn Thr Tyr Thr Gly Gln Ser Thr Tyr Ala Asp Asp Phe  
50 55 60

Lys Glu Arg Phe Ala Phe Ser Leu Glu Thr Ser Ala Thr Thr Ala His  
65 70 75 80

Leu Gln Ile Asn Asn Leu Arg Asn Glu Asp Ser Ala Thr Tyr Phe Cys  
85 90 95

Ala Arg Arg Phe Gly Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Ser  
100 105 110

Val Ser Ala Ser Ile Ser Ser Ser Gly Ser Ser Ser Gly Ser  
115 120 125

Ser Ser Ser Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu  
130 135 140

Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg Ala Ser Gln  
145 150 155 160

Asp Ile Gly Asn Ser Leu Thr Trp Leu Gln Gln Glu Pro Asp Gly Thr  
165 170 175

Ile Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Asp Ser Gly Val Pro  
180 185 190

Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile  
195 200 205

Ser Ser Leu Glu Ser Glu Asp Phe Val Val Tyr Tyr Cys Leu Gln Tyr  
210 215 220

Ala Ile Phe Pro Tyr Thr Phe Gly Gly Gly Thr Asn Leu Glu Ile Lys  
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Arg Ala Asp

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<212> PRT  
<213> Artificial sequence

<220>  
<223> Linker 1

<400> 7



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<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Linker 2

<400> 8

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<212> PRT  
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<223> C-terminal tail

<400> 9

Ser Cys  
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<210> 10  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> C-terminal tail

<400> 10

Gly Gly Gly Gly Cys  
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<210> 11  
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<212> PRT  
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<220>  
<223> C-terminal tail

<400> 11

His His His His His Gly Gly Gly Gly Cys  
1 5 10

<210> 12  
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<212> PRT  
<213> Mus musculus

<400> 12

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Gln Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Glu Pro Gly Ala  
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Ser Val Arg Ile Ser Cys Thr Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30

Tyr Ile His Trp Leu Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Phe  
65 70 75 80

Asn Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys  
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr  
100 105 110

Leu Thr Val Ser Ser Lys  
115

<210> 13  
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<212> PRT  
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<400> 13

Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly Ala  
1 5 10 15

Ser Val Arg Met Ser Cys Lys Ser Ser Gly Tyr Ile Phe Thr Asp Phe  
20 25 30

Tyr Met Asn Trp Val Arg Gln Ser His Gly Lys Ser Leu Asp Tyr Ile  
35 40 45

Gly Tyr Ile Ser Pro Tyr Ser Gly Val Thr Gly Tyr Asn Gln Lys Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys  
85 90 95

# CIBT-P01-130SequenceListing

Ala Gly Ser Ser Gly Asn Lys Trp Ala Met Asp Tyr Trp Gly His Gly  
100 105 110

Ala Ala Ser Val Thr Val Ser Ser  
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Ser Val Arg Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr  
20 25 30

Tyr Ile His Trp Leu Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile  
35 40 45

Gly Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe  
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr  
65 70 75 80

Met Glu Leu Arg Ser Leu Thr Ser Glu Cys Ser Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Tyr Thr His Tyr Tyr Phe Asp Tyr Trp Gly His Gly Ala Ser  
100 105 110

Val Thr Val Ser Ser  
115

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<220>  
<223> Hybrid peptide

<400> 15

Glu Val Gln Leu Gln Gln Ser Gly Pro Gly Leu Val Arg Pro Ser Gln  
1 5 10 15

# CIBT-P01-130SequenceListing

Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Thr Asn Tyr  
20 25 30

Tyr Ile His Trp Leu Lys Gln Pro Pro Gly Arg Leu Glu Trp Ile Gly  
35 40 45

Trp Ile Tyr Pro Gly Asn Gly Asn Thr Lys Tyr Asn Glu Asn Phe Lys  
50 55 60

Gly Arg Val Thr Met Leu Val Asp Thr Ser Lys Asn Gln Phe Ser Leu  
65 70 75 80

Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala  
85 90 95

Arg Tyr Thr His Tyr Tyr Phe  
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<210> 16  
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<212> PRT  
<213> Mus musculus

<400> 16

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Thr Leu Ser Leu Thr Cys Thr Val Ser Gly Ser Thr Phe Ser Asn Asp  
20 25 30

Tyr Tyr Thr Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile  
35 40 45

Gly Tyr Val Phe Tyr His Gly Thr Ser Asp Asp Thr Thr Pro Leu Arg  
50 55 60

Ser Arg Val Thr Met Leu Val Asp Thr Ser Ser Lys Asn Gln Phe Ser  
65 70 75 80

Leu Arg Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Arg Asn Leu Ile Ala Gly Cys Ile Asp Val Trp Gly Gln Gly Ser  
100 105 110

Leu Val Thr Val Ser Ser  
115